

Entrez Gene Name	Symbol	Accession	FID/IS (Ratio)						Location						
			1	p-val(1)	2	p-val(2)	3	p-val(3)		4	p-val(4)	5	p-val(5)	6	p-val(6)
3-oxoacid CoA transferase 1	OXC1T1	B2GV06	0.95	0.45	1.03	0.67	1.75	0.00	1.16	0.02	1.58	0.00	1.04	0.58	Cytoplasm
acyl-CoA acyltransferase 1	P17784	ACAT1	0.93	0.13	0.93	0.16	2.41	0.00	1.12	0.02	1.15	0.00	1.03	0.68	Cytoplasm
acetylase 2, mitochondrial	AC02	Q9ER34	0.93	0.02	0.99	0.86	1.79	0.00	1.23	0.00	1.74	0.00	1.00	0.95	Cytoplasm
actin related protein 2/3 complex, subunit 3, 21kDa	ARPC3	F1LR8L	0.96	0.62	1.06	0.53	1.34	0.04	0.95	0.52	1.21	0.10	0.96	0.60	Cytoplasm
actin related protein 2/3 complex, subunit 5, 16kDa	ARPC5	Q4KL78	1.05	0.57	1.09	0.39	1.36	0.09	0.98	0.70	1.20	0.04	0.98	0.75	Cytoplasm
actin, beta	ACTB	P60711						1.01	0.79	1.54	0.00	1.01	0.95	Cytoplasm	
actinin, alpha 4	ACTN4	Q9OXQ0	0.95	0.50	1.00	1.00	1.11	0.57	0.94	0.45	1.28	0.01	0.97	0.56	Cytoplasm
acyl-CoA synthetase bubblegum family member 1	ACSB1	Q924N5	0.92	0.28	0.97	0.62	1.26	0.00	1.02	0.82	1.24	0.10	1.01	0.94	Cytoplasm
acyl-CoA thioesterase 7	ACOT7	Q64559	1.13	0.31	1.18	0.20	1.86	0.03	0.88	0.26	1.74	0.01	0.87	0.16	Plasma Membrane
ADAM metalloproteinase domain 11	ADAM11	D4A6L1	1.03	0.72	0.98	0.79	1.90	0.29	0.86	0.30	0.77	0.04	1.00	0.98	Plasma Membrane
ADAM metalloproteinase domain 22	ADAM22	F1M542	1.08	0.28	0.97	0.65	0.78	0.01	0.90	0.14	0.87	0.08	1.19	0.09	Plasma Membrane
ADAM metalloproteinase domain 23	ADAM23	D3ZT36						0.92	0.14	0.79	0.03	1.18	0.03	Plasma Membrane	
adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 1	APPL1	D3ZWA8	1.19	0.13	1.21	0.09	1.49	0.01						Cytoplasm	
adaptor-related protein complex 1, beta 1 subunit	AP2B1	CS9V96	0.95	0.69	1.04	0.74	1.28	0.21	0.97	0.63	1.55	0.00	1.03	0.60	Cytoplasm
adaptor-related protein complex 2, alpha 2 subunit	AP2A2	P18484						0.95	0.32	1.31	0.00	0.91	1.00	Cytoplasm	
adaptor-related protein complex 2, sigma 1 subunit	AP2S1	P62744	0.91	0.38	0.84	0.38	1.33	0.34	0.92	0.17	1.42	0.00	1.02	0.74	Cytoplasm
adducin 1 (alpha)	ADD1	Q63028	0.97	0.52	1.01	0.88	1.45	0.00	1.07	0.32	1.65	0.01	0.94	0.25	Cytoplasm
adducin 3 (gamma)	ADD3	CS9V97						1.15	0.14	1.54	0.05	1.01	0.83	Cytoplasm	
adenylate kinase 3	AK3	Q6P2A5						1.13	0.06	1.48	0.00	0.99	0.89	Cytoplasm	
ADP-ribosylation factor 3	ARF3	P61206	1.05	0.41	1.09	0.12	1.64	0.00	0.79	0.02	1.59	0.07	0.81	0.28	Cytoplasm
ADP-ribosylation factor 5	ARF5	P64083						0.95	0.58	1.28	0.03	1.01	0.97	Cytoplasm	
aggrexin	ACAN	D4A7Y1						0.97	0.57	0.85	0.07	1.32	0.02	Extracellular Space	
aldo-keto reductase family 1, member A1 (aldehyde reductase)	AKR1A1	P51635						0.88	0.32	1.85	0.01	0.91	0.31	Cytoplasm	
aldolase C, fructose-bisphosphate	ALDOC	P08117	1.15	0.01	1.26	0.00	1.92	0.00	0.91	0.08	1.55	0.00	0.97	0.47	Cytoplasm
amphiphysin	AMPH	Q08839	1.09	0.10	1.12	0.03	1.98	0.00	1.34	0.01	0.97	0.06	0.96	0.56	Plasma Membrane
apolipoprotein E	APOE	Q6PAH0	1.20	0.10	1.11	0.09	1.29	0.00	0.96	0.33	1.11	0.16	1.05	0.30	Extracellular Space
aquaporin 4	AQP4	F47863	0.89	0.14	0.92	0.31	0.71	0.04	0.88	0.18	0.74	0.12	1.07	0.69	Plasma Membrane
ARF2 actin-related protein 2 homolog (yeast)	ACTR2	CSM7U6	0.98	0.62	1.08	0.46	1.25	0.01	0.97	0.48	1.13	0.31	1.05	0.64	Plasma Membrane
asparaginyl-tRNA synthetase	NARS	F1LVR9	0.94	0.94	1.07	0.62	1.54	0.04						Cytoplasm	
ATP citrate lyase	ACLY	G3V9G4	1.14	0.06	1.35	0.00	1.67	0.00	0.84	0.00	0.99	0.69	1.01	0.69	Cytoplasm
ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle	ATP5A1	P15999	0.89	0.00	0.98	0.48	0.89	0.25	1.28	0.00	0.86	0.00	0.93	0.02	Cytoplasm
ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide	ATP5B	G3VD03	0.86	0.00	0.95	0.15	0.84	0.00	1.28	0.00	0.86	0.00	0.91	0.01	Cytoplasm
ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	ATP5D	G3V7Y3						0.90	0.02	0.78	0.00	0.93	0.07	Cytoplasm	
ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide	ATP5G1	Q6PCL0	0.88	0.01	0.95	0.21	0.86	0.01	1.27	0.00	0.92	0.23	0.97	0.54	Cytoplasm
ATP synthase, H+ transporting, mitochondrial Fo complex, subunit B1	ATP5F1	P19511	0.86	0.02	0.92	0.15	0.81	0.01	1.29	0.00	0.99	0.85	1.04	0.41	Cytoplasm
ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	ATP2A2	E9FSX6	1.04	0.19	0.98	0.43	0.90	0.02						Cytoplasm	
ATPase, Ca++ transporting, plasma membrane 4	D4A122	P08117	1.09	0.00	1.14	0.00	0.99	0.69	0.87	0.01	0.80	0.04	0.94	0.32	Plasma Membrane
ATPase, Na+/K+ transporting, alpha 1 polypeptide	ATP1A1	P06685	0.96	0.25	0.93	0.19	0.80	0.00	0.85	0.00	0.73	0.00	1.02	0.54	Plasma Membrane
ATPase, Na+/K+ transporting, alpha 2 polypeptide	ATP1A2	P06686						0.88	0.00	0.64	0.00	0.97	0.38	Plasma Membrane	
AU RNA binding protein/enoyl-CoA hydratase	AUH	F1LUT1	0.91	0.20	0.97	0.64	1.52	0.00	1.13	0.07	0.85	0.06	0.99	0.81	Cytoplasm
BAN1-associated protein	BANP2	Q6GMN2						0.90	0.02	0.76	0.00	0.75	0.07	1.03	Cytoplasm
basigin (Ok blood group)	BSG	Q6G774	0.87	0.25	0.85	0.18	0.71	0.09	0.85	0.03	0.83	0.01	0.98	0.88	Plasma Membrane
cadherin 2, type 1, N-cadherin (neuronal)	CDH2	G3V803	1.01	0.91	0.99	0.88	0.84	0.01	0.90	0.06	0.78	0.00	1.06	0.33	Plasma Membrane
cadherin 8, type 2 (T1-cadherin)	CDH9	D3ZFC5						0.86	0.07	0.74	0.01	0.90	0.50	Plasma Membrane	
calcium channel, voltage-dependent, N type, alpha 1B subunit	CAV2B1	Q90808						0.86	0.07	0.74	0.01	0.90	0.50	Plasma Membrane	
calcium/calmodulin-dependent protein kinase II alpha	CAMK2A	P11275	1.67	0.00	1.26	0.00	1.11	0.25	0.81	0.00	0.83	0.00	1.55	0.00	Cytoplasm
calcium/calmodulin-dependent protein kinase II gamma	CAMK2G	P11730	1.57	0.00	1.33	0.00	1.12	0.12	0.89	0.17	0.89	0.17	1.33	0.13	Cytoplasm
calcium/calmodulin-dependent protein kinase II, beta	CAMK2B	G3V9C3	1.69	0.00	1.24	0.00	1.09	0.23	0.85	0.01	0.77	0.01	1.43	0.03	Cytoplasm
calnexin	CANX	P35565						1.07	0.36	0.77	0.00	1.13	0.06	Cytoplasm	
calpain 5	CAPN5	G3V7U6	0.96	0.88	0.93	0.78	0.85	0.57	0.96	0.40	0.87	0.05	1.14	0.10	Cytoplasm
catelin	CALR	P18418	0.94	0.15	0.94	0.10	0.88	0.01	1.12	0.02	0.87	0.01	1.21	0.00	Cytoplasm
CAP, adenylate cyclase-associated protein 1 (yeast)	CAP1	D08163	1.01	0.08	1.22	0.22	1.33	0.23	0.92	0.13	0.82	0.00	0.87	0.87	Plasma Membrane
capping protein (actin filament) muscle Z-line, beta	CAPZB	Q5JK32	0.98	0.68	0.96	0.41	1.13	0.05	1.06	0.40	1.25	0.02	0.99	0.82	Cytoplasm
catenin (cadherin-associated protein), beta 1, 88kDa	CTNNB1	G9WU82	1.06	0.10	0.99	0.73	0.93	0.09	0.96	0.22	0.87	0.05	1.04	0.26	Nucleus
catenin (cadherin-associated protein), delta 2	CTNND2	F1M9E6	1.08	0.21	1.01	0.85	0.94	0.34	0.99	0.85	0.83	0.02	1.07	0.14	Plasma Membrane
CD47 molecule	CD47	P97829						0.82	0.23	1.38	0.04	1.05	0.50	Plasma Membrane	
CDGSH iron sulfur domain 1	CISD1	B0K020	0.92	0.21	0.96	0.53	0.86	0.04	1.13	0.11	1.10	0.10	0.95	0.35	Cytoplasm
chaperonin containing TCP1, subunit 7 (eta)	CC77	D4AC23	1.19	0.03	1.14	0.08	1.15	0.06	0.72	0.02	0.93	0.44	0.86	0.06	Cytoplasm
citrate synthase	CS	G3V936	0.94	0.23	1.02	0.59	0.79	0.00	1.23	0.00	1.46	0.00	1.10	0.02	Cytoplasm
clathrin, heavy chain (Hc)	CLTC	F1M779	0.82	0.00	1.00	0.82	0.90	0.00	0.95	0.02	0.82	0.00	0.96	0.97	Plasma Membrane
clathrin, light chain A	CLTA	P08081	0.85	0.02	1.00	0.98	2.15	0.00	0.98	0.69	2.81	0.00	0.92	0.40	Plasma Membrane
clathrin, light chain B	CLTB	P08082	0.83	0.01	1.03	0.63	2.12	0.00	0.95	0.67	2.45	0.01	0.81	0.09	Plasma Membrane
complexin 2	CPX2	P64087	1.05	0.56	1.04	0.67	0.90	0.00						Cytoplasm	
cortactin 1	CTN1	Q6S198	0.99	0.79	1.00	1.00	0.83	0.00	0.84	0.00	1.08	0.00	1.10	0.00	Plasma Membrane
cortactin 2	CTN2	Q6H812	0.91	0.30	0.98	0.84	1.20	0.16	1.12	0.22	1.50	0.03	1.01	0.92	Plasma Membrane
creatine kinase, brain	CKB	P07335	1.23	0.00	1.27	0.00	2.18	0.00	0.77	0.00	0.90	0.00	0.83	0.03	Cytoplasm
creatine kinase, mitochondrial 1, ubiquitous	CKMT1	G58179	0.86	0.00	0.96	0.36	0.85	0.00	1.12	0.01	1.52	0.06	0.88	0.08	Cytoplasm
cytochrome b5 reductase 3	CYBR3	P20070	0.83	0.01	0.84	0.05	0.84	0.05	0.94	0.01	0.84	0.00	1.08	0.06	Cytoplasm
cytochrome c oxidase subunit IV isoform 1	COX4I1	P10888	0.90	0.03	0.98	0.64	0.85	0.01	1.23	0.02	0.84	0.02	0.93	0.16	Plasma Membrane
cytochrome c oxidase subunit Va	COX5A	P11240	0.97	0.60	1.04	0.57	0.91	0.17	1.33	0.01	0.82	0.13	0.89	0.20	Cytoplasm
cytochrome c oxidase subunit Vb	COX5B	P12075	0.96	0.66	0.97	0.66	0.85	0.17	1.30	0.05	0.76	0.00	0.91	0.22	Cytoplasm
cytochrome c oxidase subunit VIIb polypeptide 1 (ubiquitous)	COX7B1	D3ZD09	0.90	0.15	1.00	0.95	0.84	0.11	1.28	0.02	0.84	0.13	0.84	0.21	Cytoplasm
cytochrome c oxidase subunit VIc	COX6C	P11951	0.93	0.24	1.01	0.88	0.82	0.01	1.29	0.01	0.84	0.02	0.94	0.55	Cytoplasm
cytochrome c oxidase subunit VIIa polypeptide 2 like	COX7A2L	B2R7Y5	0.88	0.08	0.94	0.36	0.82								

heat shock protein 90kDa beta (Grp94), member 1	HSP90B1	Q6H0D0	0.99	0.72	0.97	0.45	0.83	0.00	1.08	0.04	0.80	0.00	1.07	0.09	Cytoplasm
heterogeneous nuclear ribonucleoprotein K	HNRNPCK	Q5D059	1.15	0.25	1.26	0.12	1.59	0.04							Nucleus
huntingtin	HTT	PS1111	0.99	0.89	1.10	0.37	0.47	0.05							Cytoplasm
hydroxyacyl-CoA dehydrogenase 3-ketocacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), beta subunit	HADHB	Q60587	0.99	0.94	1.05	0.54	0.98	0.89	1.12	0.03	0.91	0.20	0.90	0.05	Cytoplasm
hydropolization activated cyclic nucleotide-gated potassium channel 1	HCN1	F1LSH6	0.93	0.28	0.91	0.18	0.78	0.01	1.00	1.00	0.87	0.23	1.02	0.83	Plasma Membrane
hypoxanthine phosphoribosyltransferase 1	HPRT1	F1LNY0	1.14	0.26	1.16	0.22	1.80	0.16	0.86	0.08	1.59	0.02	0.85	0.02	Cytoplasm
importin 5	IP05	D44781	0.97	0.78	1.13	0.27	1.34	0.04	1.06	0.59	0.97	0.12	0.92	0.87	Nucleus
importin 1,4,5-trisphosphate receptor, type 1	ITPR1	P29948-8	0.99	0.70	0.90	0.01	0.84	0.00	1.04	0.37	0.83	0.01	1.06	0.22	Cytoplasm
inositol-trisphosphate 3-kinase A	ITPKA	P17105							1.02	0.82	1.47	0.02	1.04	0.79	Cytoplasm
inositol(myo-)(or 4-)monophosphatase 1	IMPA1	F1M978							0.95	0.76	1.59	0.00	0.96	0.59	Cytoplasm
isocitrate dehydrogenase 3 (NAD+) alpha	IDH3A	F1LNF7	0.92	0.10	0.98	0.74	1.52	0.00	1.35	0.00	1.76	0.00	0.97	0.72	Cytoplasm
isocitrate dehydrogenase 3 (NAD+) beta	IDH3B	Q68X00	0.92	0.11	1.01	0.80	1.51	0.00	1.37	0.00	1.73	0.00	1.09	0.27	Cytoplasm
isocitrate dehydrogenase 3 (NAD+) gamma	IDH3G	Q5XJL3	0.92	0.18	0.93	0.69	1.50	0.00	1.28	0.01	1.62	0.00	1.06	0.28	Cytoplasm
kallin, RhoGEF kinase domain containing	KALRN	P97524	1.09	0.07	0.92	0.07	0.78	0.42	1.06	0.21	0.91	0.22	1.28	0.00	Cytoplasm
karyopherin (importin) beta 1	KPNB1	F22308	0.97	0.72	1.07	0.53	1.32	0.24	1.00	0.99	1.51	0.03	0.91	0.40	Nucleus
lactate dehydrogenase A	LDHA	B5DEN4	1.15	0.01	1.15	0.01	0.99	0.00	0.83	0.01	1.70	0.00	0.89	0.05	Cytoplasm
lactate dehydrogenase B	LDHB	F42123	1.09	0.23	1.21	0.01	0.78	0.00	0.79	0.02	1.63	0.00	0.87	0.06	Cytoplasm
leucine rich repeat and Ig domain containing 1	LINGO1	G3V681	1.01	0.87	0.93	0.24	0.77	0.01	0.91	0.14	0.52	0.09	0.96	0.52	Plasma Membrane
low density lipoprotein receptor-related protein 1	LRP1	G3V928	1.15	0.00	1.14	0.00	0.98	0.72	0.91	0.02	0.83	0.05	1.02	0.69	Plasma Membrane
macrophage migration inhibitory factor (glycosylation-inhibiting factor)	MIF	P30904	1.20	0.19	1.35	0.08	2.47	0.01	0.84	0.19	2.05	0.01	0.89	0.28	Extracellular Space
malate dehydrogenase 1, NAD (soluble)	MDH1	O89899	1.13	0.01	1.14	0.01	1.99	0.00	0.85	0.02	1.81	0.01	0.93	0.37	Cytoplasm
malate dehydrogenase 2, NAD (mitochondrial)	MDH2	P04635	0.93	0.06	1.06	0.12	2.15	0.00	1.23	0.00	1.90	0.00	0.99	0.76	Cytoplasm
malic enzyme 1, NAD(P+)-dependent, cytosolic	ME1	P13697							0.91	0.23	1.48	0.01	0.92	0.25	Cytoplasm
malic enzyme 3, NAD(P+)-dependent, mitochondrial	ME3	F1M5N4	0.84	0.01	0.89	0.07	1.58	0.00	0.93	0.02	1.56	0.02	1.18	0.02	Cytoplasm
microtubule-associated protein 2	MAP2	F15146-2							0.93	0.02	0.96	0.45	1.04	0.15	Plasma Membrane
microtubule-associated protein tau	MAPT	F1LST4	1.13	0.09	1.11	0.14	1.73	0.00	1.04	0.63	1.32	0.02	1.10	0.06	Plasma Membrane
microtubule-associated protein, RP/EIE family, member 3	MAPRE3	Q5X1T1							0.96	0.59	1.42	0.04	0.96	0.87	Cytoplasm
mitochondrial calcium uptake 1	MCU1	Q6P909							1.16	0.04	0.91	0.32	1.02	0.80	Cytoplasm
mitogen-activated protein kinase 1	MAPK1	P63086							1.00	0.99	1.54	0.00	0.87	0.09	Cytoplasm
mitogen-activated protein kinase kinase 1	MAP2K1	Q01986	1.11	0.04	1.18	0.01	1.43	0.00	0.91	0.12	1.34	0.03	0.92	0.58	Cytoplasm
monamine oxidase A	MAOA	G3V923	0.93	0.13	0.94	0.19	0.96	0.37	1.20	0.00	0.96	0.31	1.04	0.42	Cytoplasm
monamine oxidase B	MAOB	F1FLPM4	1.06	0.34	1.08	0.51	0.95	0.38	1.15	0.02	0.93	0.39	0.92	0.10	Cytoplasm
N-ethylmaleimide-sensitive factor attachment protein, alpha	NSF	F1LC81	0.99	0.63	0.97	0.22	1.63	0.00	0.97	0.12	1.58	0.00	1.05	0.01	Cytoplasm
N-ethylmaleimide-sensitive factor attachment protein, beta	NAPB	P64921	0.8	0.18	0.97	0.56	1.20	0.01	0.86	0.07	1.61	0.01	0.92	0.39	Cytoplasm
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12	NDUFA12	F1LXAA0	0.90	0.09	0.98	0.68	0.93	0.20	1.24	0.01	0.87	0.04	0.95	0.36	Cytoplasm
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa	NDUFA2	D32538	0.99	0.05	0.74	0.11	0.85	0.03	1.22	0.03	1.22	0.03	0.93	0.25	Cytoplasm
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa	NDUFA5	Q53362	0.89	0.16	0.92	0.28	0.81	0.03	1.22	0.03	0.78	0.10	0.95	0.40	Cytoplasm
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa	NDUFA9	Q58K63	0.91	0.01	0.94	0.07	0.80	0.00	1.25	0.00	1.07	0.06	0.97	0.49	Cytoplasm
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa	NDUFB10	D44070	0.92	0.10	0.95	0.29	0.87	0.02	1.24	0.01	0.83	0.05	0.94	0.24	Cytoplasm
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa	NDUFB2	D44565	0.94	0.39	1.00	0.99	0.94	0.64	1.28	0.01	0.94	0.02	0.97	0.58	Cytoplasm
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa	NDUFB7	D3ZL71	1.02	0.84	0.99	0.92	0.91	0.39	1.22	0.03	0.91	0.19	0.88	0.80	Cytoplasm
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa	NDUFB9	B8RYV3	0.90	0.05	0.98	0.62	0.87	0.08	1.25	0.01	0.90	0.23	0.95	0.33	Cytoplasm
NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	NDUF51	Q6HFH1	0.89	0.00	0.96	0.21	0.87	0.00	1.23	0.00	0.89	0.00	0.95	0.06	Cytoplasm
NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase)	NDUF52	D34YV2	0.88	0.05	0.93	0.44	0.84	0.00	0.97	0.03	0.87	0.03	0.94	0.26	Cytoplasm
NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)	NDUF53	D3ZG43	0.92	0.11	0.96	0.44	0.80	0.00	1.23	0.00	0.87	0.04	0.92	0.30	Cytoplasm
NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)	NDUF54	Q5X1F3	0.89	0.06	0.94	0.26	0.78	0.00	1.30	0.01	0.88	0.22	0.97	0.86	Cytoplasm
NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)	NDUF58	B89N68	0.89	0.07	0.97	0.61	0.83	0.01	1.22	0.02	0.91	0.30	0.93	0.21	Cytoplasm
NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa	NDUFB1	Q01068	0.90	0.01	0.96	0.24	0.96	0.00	1.17	0.96	0.94	0.08	0.93	0.25	Cytoplasm
NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa	NDUFB2	P19234	0.86	0.04	0.96	0.51	0.85	0.02	1.26	0.02	0.95	0.57	0.99	0.92	Cytoplasm
NCK-associated protein 1	NCKAP1	P55181	1.05	0.31	1.02	0.63	1.34	0.00	0.86	0.01	1.01	0.78	1.07	0.18	Plasma Membrane
neural cell adhesion molecule 1	NCAM1	F1LUV9	1.05	0.53	1.01	0.94	0.86	0.27	1.13	0.19	0.76	0.02	1.28	0.12	Plasma Membrane
neurofilament, heavy polypeptide	NEFH	F1LR27							1.24	0.00	0.68	0.00	1.16	0.00	Cytoplasm
neurofilament, light polypeptide	NEFL	F19527	1.05	0.16	0.98	0.70	0.83	0.00	1.27	0.00	0.54	0.00	1.16	0.02	Cytoplasm
neurotrophic tyrosine kinase, receptor, type 3	NTRK3	Q03335	1.03	0.76	0.87	0.18	0.81	0.03	0.91	0.25	0.85	0.11	1.07	0.41	Plasma Membrane
optic atrophy 1 (autosomal dominant)	OPA1	D27468-3	0.95	0.06	0.98	0.38	0.82	0.00	1.07	0.00	0.92	0.03	0.95	0.55	Cytoplasm
ornithine aminotransferase	OAT	P04182							1.24	0.08	0.57	0.02	0.99	0.85	Cytoplasm
parkinson 7	PARK7	O88767	1.07	0.34	1.18	0.07	1.78	0.01	0.84	0.04	1.88	0.00	0.82	0.03	Nucleus
peptidylprolyl isomerase A (cyclophilin A)	PP1A	P10111							0.88	0.08	2.26	0.00	0.81	0.07	Cytoplasm
peptidylprolyl isomerase D	PP1D	Q60G50							0.88	0.08	2.26	0.00	0.81	0.07	Cytoplasm
peroxiredoxin 1	PRDX1	Q63716	1.05	0.45	1.09	0.19	1.38	0.01	1.06	0.33	1.37	0.01	1.03	0.62	Cytoplasm
peroxiredoxin 2	PRDX2	F95704	1.14	0.27	1.28	0.11	1.99	0.02	0.93	0.23	1.39	0.08	0.98	0.66	Cytoplasm
peroxiredoxin 5	PRDX5	D3ZEM5	0.97	0.45	1.01	0.65	0.87	0.00	1.11	0.10	0.78	0.03	0.97	0.63	Cytoplasm
peroxiredoxin 6	PRDX6	Q35244	1.08	0.25	1.16	0.49	1.00	0.00	0.83	0.03	1.78	0.00	0.78	0.11	Cytoplasm
phosphatidic acid phosphatase type 2B	PPP2B2	P97544	1.02	0.88	1.03	0.73	0.77	0.11	0.89	0.15	0.64	0.01	0.95	0.45	Plasma Membrane
phosphatidylinositol-3-OH kinase binding protein 1	P108B1	P91044	1.08	0.22	1.12	0.15	2.05	0.00	0.88	0.24	0.82	0.01	0.94	0.37	Cytoplasm
phosphodiesterase 2A, GMP-stimulated	PDE2A	P01268	0.94	0.20	0.91	0.02	0.96	0.00	1.00	0.00	0.97	0.01	1.01	0.29	Cytoplasm
phosphofructokinase, muscle	PFKM	Q5ZK51	1.21	0.00	1.22	0.00	1.85	0.00	0.87	0.02	1.22	0.00	0.95	0.23	Cytoplasm
phosphofructokinase, platelet	PFKP	F7C572	1.18	0.02	1.29	0.03	1.69	0.00	0.94	0.27	1.61	0.00	1.01	0.84	Cytoplasm
phosphoglycerate dehydrogenase	PHGDH	O08651	1.09	0.30	1.20	0.06	1.50	0.03	0.91	0.21	1.23	0.01	0.87	0.32	Cytoplasm
phosphoglycerate kinase	PFKB1	P16817							0.94	0.00	0.76	0.00	0.97	0.78	Cytoplasm
phospholipase C, beta 1 (phosphoinositide-specific)	PLCBB1	P10687	1.21	0.08	1.17	0.11	1.68	0.01	0.72	0.03	1.19	0.37	0.98	0.76	Cytoplasm
phosphoprotein enriched in astrocytes 15	PEA15	Q5U318	1.10	0.42	1.19	0.18	2.08	0.02							Cytoplasm
phosphoribosyl pyrophosphate synthetase 1	PPRS1	P60982	1.14	0.20											

solute carrier family 8 (sodium/calcium exchanger), member 1	SLC8A1	Q01728-2	0.94	0.19	0.90	0.06	0.73	0.52	0.95	0.54	0.67	0.01	1.15	0.13	Plasma Membrane
solute carrier family 8 (sodium/calcium exchanger), member 2	SLC8A2	P46768	1.00	0.93	0.94	0.13	0.78	0.00	0.81	0.01	0.61	0.00	1.02	0.79	Cytoplasm
spectrin, alpha, non-erythrocytic 1	SPTAN1	P16986							1.22	0.00	0.91	0.00	1.00	0.81	Plasma Membrane
spectrin, beta, erythrocytic	SPTB	F1MAL3	1.18	0.01	1.03	0.77	0.99	0.83	1.03	0.63	0.67	0.01	0.99	0.82	Plasma Membrane
spectrin, beta, non-erythrocytic 1	SPTBN1	G3V650	1.00	0.81	0.99	0.35	1.08	0.00	1.18	0.00	0.94	0.00	1.03	0.11	Plasma Membrane
spectrin, beta, non-erythrocytic 2	SPTBN2	F1MA36	1.02	0.51	0.95	0.18	0.93	0.05	1.31	0.00	0.83	0.00	1.04	0.02	Cytoplasm
sphingosine-1-phosphate receptor 1	S1PR1	P46303	0.94	0.52	0.93	0.50	0.66	0.05							Plasma Membrane
stathmin 1	STMN1	P13668							0.78	0.02	1.38	0.03	0.68	0.14	Cytoplasm
stress-induced-phosphoprotein 1	STP1	C35814	1.06	0.28	1.11	0.09	1.83	0.00	0.81	0.02	1.69	0.02	0.93	0.45	Cytoplasm
succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	SDHA	C920L2	0.95	0.12	0.94	0.29	0.88	0.00							Cytoplasm
succinate dehydrogenase complex, subunit B, iron sulfur (fp)	SDHB	P21913	0.92	0.05	0.97	0.46	0.88	0.01							Cytoplasm
succinate-CoA ligase, ADP-forming, beta subunit	SUCLA2	F1LM47							1.23	0.00	1.43	0.00	0.98	0.73	Cytoplasm
succinate-CoA ligase, alpha subunit	SUCLG1	P13096	1.04	0.64	1.08	0.32	1.65	0.00	1.12	0.07	1.15	0.07	1.02	0.65	Cytoplasm
superoxide dismutase 1, soluble	SOD1	Q6LD54	1.07	0.25	1.08	0.25	1.76	0.00	0.78	0.04	1.87	0.17	0.93	0.31	Cytoplasm
superoxide dismutase 2, mitochondrial	SOD2	P07895	0.98	0.77	1.03	0.68	1.76	0.00	1.11	0.13	1.22	0.03	0.94	0.29	Cytoplasm
synapsin I	SYN1	P09951	1.03	0.54	1.02	0.87	2.13	0.00	1.63	0.00	1.85	0.00	1.17	0.00	Plasma Membrane
synapsin II	SYN2	G3V733	1.10	0.04	1.12	0.11	2.91	0.00	1.43	0.00	1.89	0.00	1.08	0.44	Plasma Membrane
synaptic Ras GTPase activating protein 1	SYNGAP1	Q9CUR6	1.08	0.25	0.95	0.43	0.79	0.04	0.90	0.26	0.77	0.09	1.03	0.69	Plasma Membrane
synuclein, alpha (non A4 component of amyloid precursor)	SNCA	P37377-2	1.18	0.06	1.15	0.07	2.03	0.00	1.02	0.75	1.50	0.02	1.00	0.98	Cytoplasm
talin 2	TLN2	D3ZT58	1.02	0.87	1.10	0.38	1.56	0.03							Nucleus
tropomyosin 1, alpha	Tpm1	P04692-5							0.92	0.09	2.18	0.03	0.87	0.15	Plasma Membrane
tubulin, alpha 4a	TUBA4A	Q5XIF6	1.09	0.44	1.22	0.15	1.68	0.02	0.75	0.03	1.40	0.00	0.89	0.10	Cytoplasm
tubulin, beta 2A class Ila	TUBB2A	P85108	1.14	0.29	1.31	0.07	1.97	0.01	0.84	0.02	1.54	0.00	0.93	0.37	Cytoplasm
tubulin, beta 3 class III	TUBB3	Q4QR84	1.15	0.11	1.26	0.03	1.91	0.00	0.84	0.27	1.50	0.03	0.85	0.46	Cytoplasm
tubulin, beta class I	TUBB	P68997	1.24	0.06	1.34	0.03	1.73	0.01	0.84	0.19	1.22	0.14	0.77	0.21	Cytoplasm
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	YWHAH	P33213	0.94	0.40	1.02	0.78	1.45	0.02	0.96	0.39	2.08	0.00	0.92	0.52	Cytoplasm
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	YWHAE	P62260	1.05	0.28	1.10	0.04	1.74	0.00	0.96	0.33	1.76	0.01	0.94	0.25	Cytoplasm
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	YWHAH	P68511	1.02	0.72	1.11	0.16	1.52	0.00	0.98	0.84	1.63	0.03	0.85	0.12	Cytoplasm
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	YWHAQ	P61983	1.05	0.38	1.13	0.07	1.75	0.00	0.93	0.25	1.78	0.00	0.89	0.24	Cytoplasm
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	YWHAQ	P68255	1.11	0.17	1.18	0.05	1.95	0.00	0.95	0.57	1.94	0.01	0.87	0.14	Cytoplasm
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	YWHAZ	P63102	1.03	0.74	1.15	0.02	2.12	0.10	0.92	0.14	1.89	0.00	0.86	0.03	Cytoplasm
ubiquinol-cytochrome c reductase core protein I	UQCRC1	Q68FY0	0.96	0.29	1.02	0.57	0.91	0.07	1.29	0.00	0.95	0.40	0.94	0.14	Cytoplasm
ubiquinol-cytochrome c reductase core protein II	UQCRC2	P32551	0.97	0.51	1.01	0.75	0.84	0.00	1.20	0.00	0.86	0.00	0.95	0.19	Cytoplasm
ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	UQCRC3	P20769	0.91	0.19	0.99	0.85	0.86	0.02	1.21	0.00	0.97	0.01	0.99	0.82	Cytoplasm
ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	UCHL1	Q00981	1.17	0.02	1.26	0.00	2.16	0.00	0.86	0.06	1.88	0.00	0.91	0.19	Cytoplasm
ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)	USP14	Q5U2N2	1.22	0.14	1.27	0.11	1.95	0.02							Cytoplasm
ubiquitin-like modifier activating enzyme 1	UBA1	Q5U300	1.11	0.05	1.15	0.01	1.47	0.00	0.87	0.05	1.54	0.01	0.90	0.07	Cytoplasm
vasoin containing protein	VCP	P46462	1.04	0.33	1.11	0.01	1.54	0.00	0.88	0.01	1.48	0.00	0.93	0.11	Cytoplasm
VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	VAPA	Q92270	1.04	0.52	1.07	0.32	1.16	0.07	1.10	0.14	0.80	0.04	1.01	0.92	Plasma Membrane
VAMP (vesicle-associated membrane protein)-associated protein B and C	VAPB	Q9Z269							1.23	0.01	0.94	0.48	1.00	0.99	Plasma Membrane